

1) gene_678[GeneMark.hmm]316_aa-[36694]37644...

RID [QEN8J8FG016](#) (Expires on 10-20 19:12 pm)

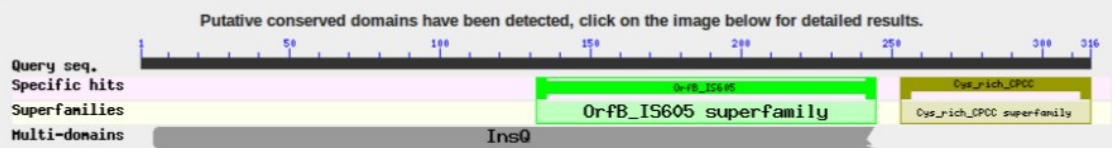
Query ID [Icd|Query_361058](#)
 Description [gene_678\[GeneMark.hmm\]316_aa-\[36694\]37644 Cry02\[50.0\]](#)
 Molecule type [amino acid](#)
 Query Length [316](#)

Database Name [nr](#)
 Description [All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects](#)
 Program [BLASTP 2.5.1+ > Citation](#)

Other reports: [Search Summary](#) [Taxonomy reports](#) [Distance tree of results](#) [Related Structures](#) [Multiple alignment](#)

Graphic Summary

Show Conserved Domains



Descriptions

Sequences producing significant alignments:

Select: [All](#) [None](#) Selected: 0

	Description	Max score	Total score	Query cover	E value	Ident	Accession
<input type="checkbox"/>	transposase [Lysinibacillus macroides]	483	483	77%	3e-169	97%	WP_053993395.1
<input type="checkbox"/>	transposase [Lysinibacillus macroides]	470	470	77%	2e-164	94%	WP_053994192.1
<input type="checkbox"/>	putative transposase family protein [Bacillus coagulans DSM 1 = ATCC 7050]	459	459	77%	4e-161	91%	AJH77703.1
<input type="checkbox"/>	transposase [Bacillus amyloliquefaciens]	458	458	77%	1e-159	91%	WP_065522509.1
<input type="checkbox"/>	transposase [Bacillus coagulans]	456	456	77%	8e-159	91%	WP_014097055.1
<input type="checkbox"/>	transposase [Bacillus coagulans]	449	449	77%	7e-156	90%	WP_042512406.1
<input type="checkbox"/>	transposase [Bacillus sp. 1NLA3E]	431	431	77%	1e-148	86%	WP_015594277.1
<input type="checkbox"/>	transposase [Bacillus coagulans]	429	429	77%	3e-148	86%	WP_013858508.1
<input type="checkbox"/>	transposase [Bacillus coagulans]	423	423	77%	1e-145	87%	WP_013858361.1
<input type="checkbox"/>	transposase [Bacillus coagulans]	419	419	77%	7e-144	86%	WP_042512402.1

2) Protein Sequence (71 letters)

RID [QENT834U01N](#) (Expires on 10-20 19:21 pm)

Query ID [Icd|Query_91838](#)
 Description [None](#)
 Molecule type [amino acid](#)
 Query Length [71](#)

Database Name [nr](#)
 Description [All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects](#)
 Program [BLASTP 2.5.1+ > Citation](#)

Other reports: [Search Summary](#) [Taxonomy reports](#) [Distance tree of results](#) [Related Structures](#) [Multiple alignment](#)

Graphic Summary

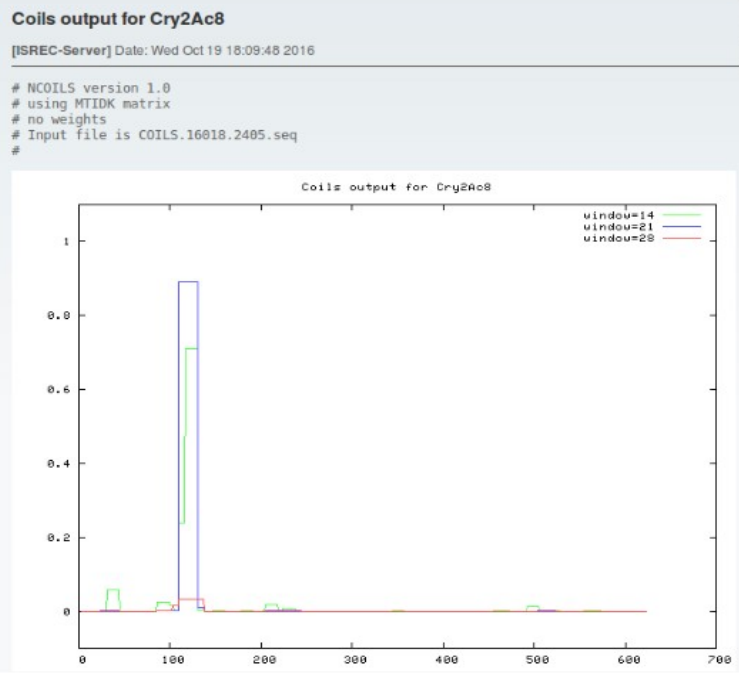
Descriptions

Sequences producing significant alignments:

Select: [All](#) [None](#) Selected: 0

	Description	Max score	Total score	Query cover	E value	Ident	Accession
<input type="checkbox"/>	hypothetical protein [Bacillus cereus]	90.1	90.1	84%	3e-22	63%	WP_061688123.1
<input type="checkbox"/>	membrane protein [Bacillus cereus]	89.4	89.4	88%	5e-22	59%	WP_000877833.1
<input type="checkbox"/>	hypothetical protein [Bacillus sp. FJAT-18017]	89.4	89.4	84%	6e-22	63%	WP_053598132.1
<input type="checkbox"/>	hypothetical protein [Bacillus cereus]	89.4	89.4	88%	7e-22	59%	WP_000877829.1
<input type="checkbox"/>	MULTISPECIES: membrane protein [Bacillus cereus group]	89.0	89.0	88%	7e-22	59%	WP_000877828.1
<input type="checkbox"/>	membrane protein [Bacillus cereus]	89.0	89.0	88%	8e-22	59%	WP_002170719.1
<input type="checkbox"/>	MULTISPECIES: membrane protein [Bacillus]	89.0	89.0	88%	8e-22	59%	WP_000877827.1
<input type="checkbox"/>	membrane protein [Bacillus cereus]	89.0	89.0	88%	9e-22	59%	WP_000877826.1
<input type="checkbox"/>	hypothetical protein [Bacillus cecembensis]	89.4	89.4	90%	1e-21	61%	WP_057982468.1
<input type="checkbox"/>	membrane protein [Kurthia massiliensis]	88.6	88.6	88%	1e-21	63%	WP_010289560.1

3)



4)

Coils output for gene_678

